

G. SEQUENCE LISTING

5 (1) GENERAL INFORMATION

(i) APPLICANT: Darrell Anderson, Nabil Hanna, John Leonard,
Roland Newman and Mitchell Reff and William H.
Rastetter

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(ii) TITLE OF INVENTION: THERAPEUTIC APPLICATION OF
CHIMERIC AND RADIOLABELED
ANTIBODIES TO HUMAN B
LYMPHOCYTE RESTRICTED
15 DIFFERENTIATION ANTIGEN FOR
TREATMENT OF B CELL LYMPHOMA

(iii) NUMBER OF SEQUENCES: 8

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(iv) CORRESPONDING ADDRESS:

(A) ADDRESSEE: IDEC Pharmaceuticals Corporation
(B) STREET: 11011 Torreyana Road
(C) CITY: San Diego
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 92121

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(v) COMPUTER READABLE FORM:

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(A) MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
(B) COMPUTER: Macintosh
(C) OPERATING SYSTEM: MS.DOS
(D) SOFTWARE: Microsoft Word 5.0

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(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

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(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Burgoon, Richard P. Jr.
(B) REGISTRATION NUMBER: 34,787
(C) REFERENCE/DOCKET NUMBER:

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(ix) TELECOMMUNICATION INFORMATION:

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(A) TELEPHONE: (619) 550-8500
(B) TELEFAX: (619) 550-8750

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8540 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: yes

(iv) ANTI-SENSE: no

(ix) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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GACGTCGCGG CCGCTCTAGG CCTCCAAAAA AGCCTCCTCA CTACTTCTGG AATAGCTCAG 60
AGGCCGAGGC GGCCTCGGCC TCTGCATAAA TAAAAAAAT TAGTCAGCCA TGCATGGGGC 120
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ATGGTTGCTG ACTAATTGAG ATGCATGCTT TGCATACTTC TGCCTGCTGG GGAGCCTGGG 240
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GGGAGCCTG GGGACTTTCC ACACCCTAAC TGACACACAT TCCACAGAAT TAATTCCCCT 360
AGTTATTAAT AGTAATCAAT TACGGGGTCA TTAGTTCATA GCCCATATAT GGAGTTCCGC 420
GTTACATAAC TTACGGTAAA TGGCCCGCCT GGCTGACCGC CCAACGACCC CCGCCCATTG 480
ACGTCAATAA TGACGTATGT TCCCATAGTA ACGCCAATAG GGACTTTCCA TTGACGTCAA 540
TGGGTGGACT ATTTACGGTA AACTGCCCAC TTGGCAGTAC ATCAAGTGTA TCATATGCCA 600
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GACTTTCCAA AATGTCGTAA CAACTCCGCC CCATTGACGC AAATGGGCGG TAGGCGTGTA 900
CGGTGGGAGG TCTATATAAG CAGAGCTGGG TACGTGAACC GTCAGATCGC CTGGAGACGC 960
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CTCCCAGGTG CACGATGTGA TGGTACCAAG GTGGAAATCA AACGTACGGT GGCTGCACCA 1080
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TGCCTGCTGA ATAACCTCTA TCCCAGAGAG GCCAAAGTAC AGTGGAAGGT GGATAACGCC 1200
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 10 GTTTGCCCCCT CCCCCGTGCC TTCCTTGACC CTGGAAGGTG CCACTCCCAC TGTCTTTCC 1560
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 15 GCGGTGGGCT CTATGGAACC AGCTGGGGCT CGACAGCTAT GCCAAGTACG CCCCTATTG 1740
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 20 GGCAGTACAT CAATGGGCGT GGATAGCGGT TTGACTCACG GGGATTCCA AGTCTCCACC 1920
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 25 GTAACAACTC CGCCCCATTG ACGCAAATGG GCGGTAGGCG TGTACGGTGG GAGGTCTATA 2040
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 30 AAGGGCCCAT CGGTCTTCCC CCTGGCACC TCCTCCAAGA GCACCTCTGG GGGCACAGCG 2220
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 35 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC 2340
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 55 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG 2940
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 60 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC 3120
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15 AGACAGTGTT CTCTGCACAG ATAAGGACAA ACATTATTCA GAGGGAGTAC CCAGAGCTGA 3660

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GTTTCGACCAT TGAAGTGCAT CGTCGCCGTG TCCCAAAATA TGGGGATTGG CAAGAACGGA 4020

30 GACCTACCCT GGCTCCGCT CAGGAACGAG TTCAAGTACT TCCAAAGAAT GACCACAACC 4080

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	TTGTGTTGGG	AGCTTGGATC	GATCCTCTAT	GGTTGAACAA	GATGGATTGC	ACGCAGGTTT	5280
10	TCCGGCCGCT	TGGGTGGAGA	GGCTATTGCG	CTATGACTGG	GCACAAACAG	CAATCGGCTG	5340
	CTCTGATGCC	GCCGTGTTCC	GGCTGTCAGC	GCAGGGGCGC	CCGGTTCTTT	TTGTCAAGAC	5400
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	GCTGCTATTG	GGCGAAGTGC	CGGGGCAGGA	TCTCCTGTCA	TCTCACCTTG	CTCCTGCCGA	5580
20	GAAAGTATCC	ATCATGGCTG	ATGCAATGCG	GCGGCTGCAT	ACGCTTGATC	CGGCTACCTG	5640
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25	CGCCAGGCTC	AAGGCGCGCA	TGCCCAGCGG	CGAGGATCTC	GTCGTGACCC	ATGGCGATGC	5820
	CTGCTTGCCG	AATATCATGG	TGGAAAATGG	CCGCTTTTCT	GGATTCATCG	ACTGTGGCCG	5880
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35	GAAATGACCG	ACCAAGCGAC	GCCCAACCTG	CCATCACGAG	ATTTGATTC	CACCGCCGCC	6120
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40	CGCGGGGATC	TCATGCTGGA	GTTCTTCGCC	CACCCCAACT	TGTTTATTGC	AGCTTATAAT	6240
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	TCTAGTTGTG	GTTTGTCCAA	ACTCATCAAT	CTATCTTATC	ATGTCTGGAT	CGCGGCCGCG	6360
45	ATCCCGTCGA	GAGCTTGGCG	TAATCATGGT	CATAGCTGTT	TCCTGTGTGA	AATTGTTATC	6420
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50	AATGAGTGAG	CTAACTCACA	TTAATTGCGT	TGCGCTCACT	GCCCGCTTTC	CAGTCGGGAA	6540
	ACCTGTCGTG	CCAGCTGCAT	TAATGAATCG	GCCAACGCGC	GGGGAGAGGC	GGTTTGCGTA	6600
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55	GAGCGGTATC	AGCTCACTCA	AAGGCGGTAA	TACGGTTATC	CACAGAATCA	GGGGATAACG	6720
	CAGGAAAGAA	CATGTGAGCA	AAAGGCCAGC	AAAAGGCCAG	GAACCGTAAA	AAGGCCGCGT	6780
60	TGCTGGCGTT	TTCCATAGG	CTCCGCCCCC	CTGACGAGCA	TCACAAAAAT	CGACGCTCAA	6840
	GTCAGAGGTG	GCGAAACCCG	ACAGGACTAT	AAAGATACCA	GGCGTTTCCC	CCTGGAAGCT	6900
	CCCTCGTGCG	CTCTCCTGTT	CCGACCCTGC	CGCTTACCGG	ATACCTGTCC	GCCTTTCTCC	6960

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35 CCCAACGATC AAGGCGAGTT ACATGATCCC CCATGTTGTG CAAAAAAGCG GTTAGCTCCT 7980

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CGTCAATACG GGATAATACC GCGCCACATA GCAGAACTTT AAAAGTGCTC ATCATTGGAA 8220

45 AACGTTCTTC GGGGCGAAAA CTCTCAAGGA TCTTACCGCT GTTGAGATCC AGTTCGATGT 8280

AACCCACTCG TGCACCCAAC TGATCTTCAG CATCTTTTAC TTTCAACAGC GTTCTGCGGT 8340

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50 GAATACTCAT ACTCTCCTT TTTCAATATT ATTGAAGCAT TTATCAGGGT TATTGTCTCA 8460

TGAGCGGATA CATATTTGAA TGTATTTAGA AAAATAAACA AATAGGGGTT CCGCGCACAT 8520

55 TTCCCCGAAA AGTGCCACCT 8540

(3) INFORMATION FOR SEQ ID NO: 2:

60 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9209 bases

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: circular

5 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: yes

(iv) ANTI-SENSE: no

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(ix) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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	AGGCCGAGGC GGCCTCGGCC TCTGCATAAA TAAAAAAAT TAGTCAGCCA TGCATGGGGC	120
	GGAGAATGGG CGGAAGTGGG CGGAGTTAGG GCGGGGATGG GCGGAGTTAG GGGCGGGACT	180
20	ATGGTTGCTG ACTAATTGAG ATGCATGCTT TGCATACTTC TGCCTGCTGG GGAGCCTGGG	240
	GACTTTCCAC ACCTGGTTGC TGACTAATTG AGATGCATGC TTTGCATACT TCTGCCTGCT	300
	GGGGAGCCTG GGGACTTTCC ACACCCTAAC TGACACACAT TCCACAGAAT TAATTCCCCT	360
25	AGTTATTAAT AGTAATCAAT TACGGGGTCA TTAGTTCATA GCCCATATAT GGAGTTCCGC	420
	GTTACATAAC TTACGGTAA TGGCCCGCCT GGCTGACCGC CCAACGACCC CCGCCCATTG	480
30	ACGTCAATAA TGACGTATGT TCCCATAGTA ACGCCAATAG GGACTTTCCA TTGACGTCAA	540
	TGGGTGGACT ATTTACGGTA AACTGCCCCAC TTGGCAGTAC ATCAAGTGTA TCATATGCCA	600
	AGTACGCCCC CTATTGACGT CAATGACGGT AAATGGCCCCG CCTGGCATTG TGCCAGTAC	660
35	ATGACCTTAT GGGACTTTCC TACTTGGCAG TACATCTACG TATTAGTCAT CGCTATTACC	720
	ATGGTGTATG GGTTTTGGCA GTACATCAAT GGGCGTGGAT AGCGGTTTGA CTCACGGGGA	780
40	TTTCCAAGTC TCCACCCCAT TGACGTCAAT GGGAGTTTGT TTTGGCACCA AAATCAACGG	840
	GACTTTCCAA AATGTCGTAA CAACTCCGCC CCATTGACGC AAATGGGCGG TAGGCGTGTA	900
	CGGTGGGAGG TCTATATAAG CAGAGCTGGG TACGTGAACC GTCAGATCGC CTGGAGACGC	960
45	CATCACAGAT CTCTCACTAT GGATTTTCAG GTGCAGATTA TCAGCTTCCT GCTAATCAGT	1020
	GCTTCAGTCA TAATGTCCAG AGGACAAATT GTTCTCTCCC AGTCTCCAGC AATCCTGTCT	1080
50	GCATCTCCAG GGGAGAAGGT CACAATGACT TGCAGGGCCA GCTCAAGTGT AAGTTACATC	1140
	CACTGGTTCC AGCAGAAGCC AGGATCCTCC CCCAAACCCT GGATTTATGC CACATCCAAC	1200
	CTGGCTTCTG GAGTCCCTGT TCGCTTCAGT GGCAGTGGGT CTGGGACTTC TTA CTCTCTC	1260
55	ACAATCAGCA GAGTGGAGGC TGAAGATGCT GCCACTTATT ACTGCCAGCA GTGGACTAGT	1320
	AACCCACCCA CGTTCGGAGG GGGGACCAAG CTGGAAATCA AACGTACGGT GGCTGCACCA	1380
60	TCTGTCTTCA TCTTCCCGCC ATCTGATGAG CAGTTGAAAT CTGGAAGTGC CTCTGTTGTG	1440

5 TGCCTGCTGA ATAACTTCTA TCCCAGAGAG GCCAAAGTAC AGTGGGAAGGT GGATAACGCC 1500
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 10 AGCCTCAGCA GCACCCTGAC GCTGAGCAAA GCAGACTACG AGAAACACAA AGTCTACGCC 1620
 TGCGAAGTCA CCCATCAGGG CCTGAGCTCG CCCGTCACAA AGAGCTTCAA CAGGGGAGAG 1680
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 15 GGCCGTGATA TCTACGTATG ATCAGCCTCG ACTGTGCCTT CTAGTTGCCA GCCATCTGTT 1800
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 20 GCGGTGGGCT CTATGGAACC AGCTGGGGCT CGACAGCTAT GCCAAGTACG CCCCCTATTG 2040
 ACGTCAATGA CGGTAAATGG CCCGCCTGGC ATTATGCCCA GTACATGACC TTATGGGACT 2100
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 CCATTGACGT CAATGGGAGT TTGTTTTGGC ACCAAAATCA ACGGGACTTT CCAAAATGTC 2280
 30 GTAACAACTC CGCCCCATTG ACGCAAATGG GCGGTAGGCG TGTACGGTGG GAGGTCTATA 2340
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 40 GGTGCGGGCC TGAATGGAT TGGAGCTATT TATCCCGGAA ATGGTGATAC TTCCTACAAT 2640
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 45 TACGCGGGTG ACTGGTACTT CAATGTCTGG GGCGCAGGGA CCACGGTCAC CGTCTCTGCA 2820
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 50 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCTG 2940
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 60 CCGTCAGTCT TCCTCTTCCC CCCAAAACCC AAGGACACCC TCATGATCTC CCGGACCCCT 3240
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 TACGTGGACG GCGTGGAGGT GCATAATGCC AAGACAAAGC CGCGGGAGGA GCAGTACAAC 3360

5 AGCACGTACC GTGTGGTCAG CGTCCTCACC GTCCTGCACC AGGACTGGCT GAATGGCAAG 3420
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 10 ~~CTGACGAAGA ACCAGGTCAG CCTGACCTGG GTGCTCAAAAG GCTTCTATCC CAGCGACATG~~ 3600
 GCCGTGGAGT GGGAGAGCAA TGGGCAGCCG GAGAACAACCT ACAAGACCAC GCCTCCCGTG 3660
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 15 CAGCAGGGGA ACGTCTTCTC ATGCTCCGTG ATGCATGAGG CTCTGCACAA CCACTACACG 3780
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 30 AGGAAAATTA ATTTTAACAC CAATTCAGTA GTTGATTGAG CAAATGCGTT GCCAAAAAGG 4260
 ATGCTTTAGA GACAGTGTTT TCTGCACAGA TAAGGACAAA CATTATTCAG AGGGAGTACC 4320
 35 CAGAGCTGAG ACTCCTAAGC CAGTGAGTGG CACAGCATTG TAGGGAGAAA TATGCTTGTC 4380
 ATCACCGAAG CCTGATTCCG TAGAGCCACA CCTTGGAAG GGCCAATCTG CTCACACAGG 4440
 ATAGAGAGGG CAGGAGCCAG GGCAGAGCAT ATAAGGTGAG GTAGGATCAG TTGCTCCTCA 4500
 40 CATTGCTTTC TGACATAGTT GTGTTGGGAG CTTGGATAGC TTGGACAGCT CAGGGCTGCG 4560
 ATTTGCGGCC AAAGTTGACG GCAATCCTAG CGTGAAGGCT GGTAGGATTT TATCCCCGCT 4620
 45 GCCATCATGG TTCGACCATT GAACTGCATC GTCGCCGTGT CCCAAAATAT GGGGATTGGC 4680
 AAGAACGGAG ACCTACCCTG GCCTCCGCTC AGGAACGAGT TCAAGTACTT CCAAAGAATG 4740
 ACCACAACCT CTTCAAGTGA AGGTAAACAG AATCTGGTGA TTATGGGTAG GAAAACCTGG 4800
 50 TTCTCCATTC CTGAGAAGAA TCGACCTTTA AAGGACAGAA TTAATATAGT TCTCAGTAGA 4860
 GAACTCAAAG AACCACCACG AGGAGCTCAT TTTCTTGCCA AAAGTTTGGA TGATGCCTTA 4920
 55 AGACTTATTG AACAACCGGA ATTGGCAAGT AAAGTAGACA TGGTTTGAT AGTCGGAGGC 4980
 AGTTCTGTTT ACCAGGAAGC CATGAATCAA CCAGGCCACC TTAGACTCTT TGTGACAAGG 5040
 ATCATGCAGG AATTTGAAAG TGACACGTTT TTCCAGAAA TTGATTTGGG GAAATATAAA 5100
 60 CTTCTCCAG AATACCCAGG CGTCTCTCT GAGGTCCAGG AGGAAAAAGG CATCAAGTAT 5160
 AAGTTTGAAG TCTACGAGAA GAAAGACTAA CAGGAAGATG CTTTCAAGTT CTCTGCTCCC 5220

CTCCTAAAGC TATGCATTTT TATAAGACCA TGGGACTTTT GCTGGCTTTA GATCAGCCTC 5280
GACTGTGCCT TCTAGTTGCC AGCCATCTGT TGTTCGCCCC TCCCCGTGC CTTCCCTTGAC 5340
5 CCTGGAAGGT GCCACTCCCA CTGTCCCTTC CTAATAAAAT GAGGAAATTG CATCGCATTG 5400
TCTGAGTAGG TGTCATTCTA TTCTGGGGGG TGGGGTGGGG CAGGACAGCA AGGGGGAGGA 5460
10 TTGGGAAGAC AATAGCAGGC ATGCTGGGGA TGGGGTGGGC TCTATGGAAC CAGCTGGGGC 5520
TCGAGCTACT AGCTTTGCTT CTCAATTTCT TATTTGCATA ATGAGAAAAA AAGGAAAATT 5580
AATTTTAACA CCAATTCAGT AGTTGATTGA GCAAATGCGT TGCCAAAAAG GATGCTTTAG 5640
15 AGACAGTGTT CTCTGCACAG ATAAGGACAA ACATTATTCA GAGGGAGTAC CCAGAGCTGA 5700
GACTCCTAAG CCAGTGAGTG GCACAGCATT CTAGGGAGAA ATATGCTTGT CATCACCGAA 5760
GCCTGATTCC GTAGAGCCAC ACCTTGTTAA GGGCCAATCT GCTCACACAG GATAGAGAGG 5820
20 GCAGGAGCCA GGGCAGAGCA TATAAGGTGA GGTAGGATCA GTTGCTCCTC ACATTTGCTT 5880
CTGACATAGT TGTGTTGGGA GCTTGATCG ATCCTCTATG GTTGAACAAG ATGGATTGCA 5940
25 CGCAGGTTCT CCGGCCGCTT GGGTGGAGAG GCTATTGCGC TATGACTGGG CACAACAGAC 6000
AATCGGCTGC TCTGATGCCG CCGTGTCCG GCTGTCAGCG CAGGGGCGCC CGGTTCTTTT 6060
TGTCAGACC GACCTGTCCG GTGCCCTGAA TGAAGTGCAG GACGAGGCAG CGCGGCTATC 6120
30 GTGGCTGGCC ACGACGGCGG TTCCTTGCGC AGCTGTGCTC GACGTTGTCA CTGAAGCGGG 6180
AAGGGAAGTG CTGCTATTGG GCGAAGTGCC GGGGCAGGAT CTCCTGTCAT CTCACCTTGC 6240
35 TCCTGCCGAG AAAGTATCCA TCATGGCTGA TGCAATGCGG CGGCTGCATA CGCTTGATCC 6300
GGCTACCTGC CCATTCGACC ACCAAGCGAA ACATCGCATC GAGCGAGCAC GTACTCGGAT 6360
GGAAGCCGGT CTTGTGATC AGGATGATCT GGACGAAGAG CATCAGGGGC TCGCGCCAGC 6420
40 CGAACTGTTT GCCAGGCTCA AGGCGCGCAT GCCCGACGGC GAGGATCTCG TCGTGACCCA 6480
TGCGGATGCC TGCTTGCCGA ATATCATGGT GGAAAATGGC CGCTTTTCTG GATTCATCGA 6540
45 CTGTGGCCGG CTGGGTGTGG CGGACCGCTA TCAGGACATA GCGTTGGCTA CCCGTGATAT 6600
TGCTGAAGAG CTTGGCGGCG AATGGGCTGA CCGCTTCCTC GTGCTTTACG GTATCGCCGC 6660
TCCCGATTCT CAGCGCATCG CCTTCTATCG CCTTCTTGAC GAGTTCTTCT GAGCGGGACT 6720
50 CTGGGGTTCT AAATGACCGA CCAAGCGACG CCCAACCTGC CATCACGAGA TTTCGATTCC 6780
ACCGCCGCTT TCTATGAAAG GTTGGGCTTC GGAATCGTTT TCCGGGACGC CGGCTGGATG 6840
55 ATCCTCCAGC GCGGGGATCT CATGCTGGAG TTCTTCGCCC ACCCCAATT GTTTATTGCA 6900
GCTTATAATG GTTACAAATA AAGCAATAGC ATCACAAATT TCACAAATAA AGCATTTTTT 6960
TCACTGCATT CTAGTTGTGG TTTGTCCAAA CTCATCAATC TATCTTATCA TGTCTGGATC 7020
60 GCGGCCGCGA TCCCGTCGAG AGCTTGGCGT AATCATGGTC ATAGCTGTTT CCTGTGTGAA 7080
ATTGTTATCC GCTCACAATT CCACACAACA TACGAGCCGG AAGCATAAAG TGTAAGCCT 7140

5 GGGGTGCCTA ATGAGTGAGC TAACTCACAT TAATTGCGTT GCGCTCACTG CCCGCTTTCC 7200
 AGTCGGGAAA CCTGTCGTGC CAGCTGCATT AATGAATCGG CCAACGCGCG GGGAGAGGCG 7260
 GTTTGCGTAT TGGGCGCTCT TCCGCTTCCT CGCTCACTGA CTCGCTGCGC TCGGTCGTTC 7320
 GGGTGCCTA AGCGCTATCA GCTCACTCAA AGCGCGTAAT ACCTTTATCC ACAGAAATCA 7380
 10 GGGATAACGC AGGAAAGAAC ATGTGAGCAA AAGGCCAGCA AAAGGCCAGG AACCGTAAAA 7440
 AGGCCGCGTT GCTGGCGTTT TTCCATAGGC TCCGCCCCC TGACGAGCAT CACAAAAATC 7500
 15 GACGCTCAAG TCAGAGGTGG CGAAACCCGA CAGGACTATA AAGATACCAG GCGTTTCCCC 7560
 CTGGAAGCTC CCTCGTGCGC TCTCCTGTTT CGACCCCTGCC GCTTACCGGA TACCTGTCCG 7620
 CCTTTCTCCC TTCGGGAAGC GTGGCGCTTT CTCAATGCTC ACCTGTAGG TATCTCAGTT 7680
 20 CGGTGTAGGT CGTTCGCTCC AAGCTGGGCT GTGTGCACGA ACCCCCCGTT CAGCCCCGACC 7740
 GCTGCGCCTT ATCCGGTAAC TATCGTCTTG AGTCCAACCC GGTAAGACAC GACTTATCGC 7800
 25 CACTGGCAGC AGCCACTGGT AACAGGATTA GCAGAGCGAG GTATGTAGGC GGTGCTACAG 7860
 AGTTCTTGAA GTGGTGGCCT AACTACGGCT AACTAGAAG GACAGTATTT GGTATCTGCG 7920
 CTCTGCTGAA GCCAGTTACC TTCGAAAAA GAGTTGGTAG CTCTTGATCC GGCAAAACAA 7980
 30 CCACCGCTGG TAGCGGTGGT TTTTGTGTTT GCAAGCAGCA GATTACGCGC AGAAAAAAG 8040
 GATCTCAAGA AGATCCTTTG ATCTTTTCTA CGGGGTCTGA CGCTCAGTGG AACGAAAACT 8100
 35 CACGTAAAGG GATTTTGGTC ATGAGATTAT CAAAAAGGAT CTTCACCTAG ATCCTTTTAA 8160
 ATTAAAAATG AAGTTTAAA TCAATCTAAA GTATATATGA GTAAACTTGG TCTGACAGTT 8220
 ACCAATGCTT AATCAGTGAG GCACCTATCT CAGCGATCTG TCTATTTCTG TCATCCATAG 8280
 40 TTGCCTGACT CCCCGTCGTG TAGATAACTA CGATACGGGA GGGCTTACCA TCTGGCCCCA 8340
 GTGCTGCAAT GATACCGCGA GACCCACGCT CACCGGCTCC AGATTTATCA GCAATAAACC 8400
 45 AGCCAGCCGG AAGGCCGAG CGCAGAAGTG GTCCTGCAAC TTTATCCGCC TCCATCCAGT 8460
 CTATTAATTG TTGCCGGGAA GCTAGAGTAA GTAGTTCGCC AGTTAATAGT TTGCGCAACG 8520
 TTGTGCCAT TGCTACAGGC ATCGTGGTGT CACGCTCGTC GTTGGTATG GCTTCATTCA 8580
 50 GCTCCGGTTC CCAACGATCA AGGCGAGTTA CATGATCCCC CATGTTGTGC AAAAAAGCGG 8640
 TTAGCTCCTT CGGTCCTCCG ATCGTTGTCA GAAGTAAGTT GGCCGAGTG TTATCACTCA 8700
 55 TGGTTATGGC AGCACTGCAT AATTCTCTTA CTGTCATGCC ATCCGTAAGA TGCTTTTCTG 8760
 TGACTGGTGA GTACTCAACC AAGTCATTCT GAGAATAGTG TATGCGGCGA CCGAGTTGCT 8820
 CTTGCCCCGC GTCAATACGG GATAATACCG CGCCACATAG CAGAACTTTA AAAGTGCTCA 8880
 60 TCATTGAAA ACGTCTTCG GGGCGAAAAC TCTCAAGGAT CTTACCGCTG TTGAGATCCA 8940
 GTTCGATGTA ACCCACTCGT GCACCAACT GATCTTCAGC ATCTTTTACT TTCACCAGCG 9000

TTTCTGGGTG AGCAAAAACA GGAAGGCAAA ATGCCGCAAA AAAGGGAATA AGGGCGACAC 9060
 GGAAATGTTG AATACTCATA CTCTTCCTTT TTCAATATTA TTGAAGCATT TATCAGGGTT 9120
 5 ATGTGTCTCAT GAGCGGATAC ATATTTGAAT GTATTTAGAA AAATAAACAA ATAGGGGTTC 9180
 CGCGCACATT TCCCCGAAAA GTGCCACCT 9209

10 (4) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 54 bases
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: yes

(iv) ANTI-SENSE: no

25 (ix) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

5' ATC ACA GAT CTC TCA CCA TGG ATT TTC AGG TBC AGA TTA TCA GCT 52
 TC 3' 2

30

(5) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 30 bases
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: yes

(iv) ANTI-SENSE: yes

45

(ix) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

50

5' TGC AGC ATC CGT ACG TTT GAT TTC CAG CTT 3' 30

(6) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 384 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: yes

10

(iv) ANTI-SENSE: no

(ix) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

15 ATG GAT TTT CAG GTG CAG ATT ATC AGC TTC CTG CTA ATC AGT GCT TCA GTC 51
 ATA ATG TCC AGA GGG CAA ATT GTT CTC TCC CAG TCT CCA GCA ATC CTG TCT 102
 GCA TCT CCA GGG GAG AAG GTC ACA ATG ACT TGC AGG GCC AGC TCA AGT GTA 153
 20 AGT TAC ATC CAC TGG TTC CAG CAG AAG CCA GGA TCC TCC CCC AAA CCC TGG 204
 ATT TAT GCC ACA TCC AAC CTG GCT TCT GGA GTC CCT GTT CGC TTC AGT GGC 255
 25 AGT GGG TCT GGG ACT TCT TAC TCT CTC ACA ATC AGC AGA GTG GAG GCT GAA 306
 GAT GCT GCC ACT TAT TAC TGC CAG CAG TGG ACT AGT AAC CCA CCC ACG TTC 357
 GGA GGG GGG ACC AAG CTG GAA ATC AAA 384
 30

(7) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 27 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: yes

45

(iv) ANTI-SENSE: no

(ix) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

50

5' GCG GCT CCC ACG CGT GTC CTG TCC CAG 3'

27

(8) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 29 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: yes

(iv) ANTI-SENSE: yes

15 (ix) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

5' GGS TGT TGT GCT AGC TGM RGA GAC RGT GA 3' 29

20 (9) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 420 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: yes

(iv) ANTI-SENSE: no

35 (ix) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

40 ATG GGT TGG AGC CTC ATC TTG CTC TTC CTT GTC GCT GTT GCT ACG CGT GTC 51
CTG TCC CAG GTA CAA CTG CAG CAG CCT GGG GCT GAG CTG GTG AAG CCT GGG 102
GCC TCA GTG AAG ATG TCC TGC AAG GCT TCT GGC TAC ACA TTT ACC AGT TAC 153
45 AAT ATG CAC TGG GTA AAA CAG ACA CCT GGT CGG GGC CTG GAA TGG ATT GGA 204
GCT ATT TAT CCC GGA AAT GGT GAT ACT TCC TAC AAT CAG AAG TTC AAA GGC 255
AAG GCC ACA TTG ACT GCA GAC AAA TCC TCC AGC ACA GCC TAC ATG CAG CTC 306
50 AGC AGC CTG ACA TCT GAG GAC TCT GCG GTC TAT TAC TGT GCA AGA TCG ACT 357
TAC TAC GGC GGT GAC TGG TAC TTC AAT GTC TGG GGC GCA GGG ACC ACG GTC 408
ACC GTC TCT GCA 420